



PCT

## RAW SEQUENCE LISTING

DATE: 04/03/2003

PATENT APPLICATION: US/10/030,269A

TIME: 14:28:06

Input Set : A:\217925US0XPCT.txt

Output Set: N:\CRF4\04032003\J030269A.raw

3 <110> APPLICANT: OTA, TOSHIO  
 4 ISOGAI, TAKAO  
 5 NISHIKAWA, TETSUO  
 6 HIO, YURI  
 7 YAMAZAKI, MAYAKO  
 8 SATOH, SUSUMU  
 9 ARAKAWA, HIROYUKI  
 10 MORITA, MASAHIKO  
 12 <120> TITLE OF INVENTION: AMYLOID-BETA PROTEIN AGGREGATION-REGULATING FACTORS  
 14 <130> FILE REFERENCE: 217925US0XPCT  
 16 <140> CURRENT APPLICATION NUMBER: 10/030,269A  
**C--> 17 <141> CURRENT FILING DATE: 2002-09-09**  
 19 <150> PRIOR APPLICATION NUMBER: PCT/JP00/04515  
 20 <151> PRIOR FILING DATE: 2000-07-06  
 22 <150> PRIOR APPLICATION NUMBER: JP 11-194179  
 23 <151> PRIOR FILING DATE: 1999-07-08  
 25 <150> PRIOR APPLICATION NUMBER: US 60/159,586  
 26 <151> PRIOR FILING DATE: 1999-10-18  
 28 <160> NUMBER OF SEQ ID NOS: 22  
 30 <170> SOFTWARE: PatentIn version 3.1  
 32 <210> SEQ ID NO: 1  
 33 <211> LENGTH: 1499  
 34 <212> TYPE: DNA  
 35 <213> ORGANISM: Homo sapiens  
 37 <220> FEATURE:  
 38 <221> NAME/KEY: CDS  
 39 <222> LOCATION: (58)..(606)  
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 46 atg aag ctc tta tct ttg gtg gcc gtg gtc ggg tgt ttg ctg gtg ccc 105  
 47 Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro  
 48 1 5 10 15  
 50 cca gct gaa gcc aac aag agt tct gaa gat atc cgg tgc aaa tgc atc 153  
 51 Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile  
 52 20 25 30  
 54 tgt cca cct tat aga aac atc agt ggg cat att tac aac cag aat gta 201  
 55 Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val  
 56 35 40 45  
 58 tcc cag aag gac tgc aac tgc ctg cac gtg gtg gag ccc atg cca gtg 249  
 59 Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val  
 60 50 55 60  
 62 cct ggc cat gac gtg gag gcc tac tgc ctg ctg tgc gag tgc agg tac 297

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63 Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr
64 65          70          75          80
66 gag gag cgc agc acc acc acc atc aag gtc atc att gtc atc tac ctg      345
67 Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu
68          85          90          95
70 tcc gtg gtg ggt gcc ctg ttg ctc tac atg gcc ttc ctg atg ctg gtg      393
71 Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val
72          100          105          110
74 gac cct ctg atc cga aag ccg gat gca tac act gag caa ctg cac aat      441
75 Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn
76          115          120          125
78 gag gag gag aat gag gat gct cgc tct atg gca gca gct gct gca tcc      489
79 Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ala Ser
80          130          135          140
82 ctc ggg gga ccc cga gca aac aca gtc ctg gag cgt gtg gaa ggt gcc      537
83 Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala
84 145          150          155          160
86 cag cag cgg tgg aag ctg cag gtg cag gag cag cgg aag aca gtc ttc      585
87 Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe
88          165          170          175
90 gat cgg cac aag atg ctc agc tagatgggct ggtgtggttg ggtcaaggcc      636
91 Asp Arg His Lys Met Leu Ser
92          180
94 ccaacacccat ggctgccagc ttccaggctg gacaaagcag ggggctactt ctcccttccc      696
96 tcggttccag tcttcccttt aaaagcctgt ggcatttttc ctcttctctc ctaactttag      756
98 aaatgttgta cttggctatt ttgattaggg aagaggggatg tggctctctga tctctgttgt      816
100 cttcttgggt ctttgggggt gaaggggatgg ggaaggcagg ccagaaggga atggagacat      876
102 tcgaggcggc ctcaggagtg gatgcgatct gtctctcctg gctccactct tgccgccttc      936
104 cagctctgag tcttgggaat gttgttaccc ttggaagata aagctgggtc ttcaggaact      996
106 cagtgtctgg gaggaaagca tggcccagca ttcagcatgt gttcctttct gcagtggctc      1056
108 ttatcaccac ctccctccca gccccagcgc ctcagcccca gccccagctc cagccctgag      1116
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112 agctgggtgt cgctgtcccc tgtgcacttc tcgcactggg gcatggagtg cccatgcata      1236
114 ctctgctgcc ggtccctcca cctgcacttg aggggtctgg gcagtccctc ctctccccag      1296
116 tgtccacagt cactgagcca gacggtcggt tggaacatga gactcgaggc tgagcgtgga      1356
118 tctgaacacc acagcccctg tacttggggt gcctcttgct cctgaacttc gttgtaccag      1416
120 tgcattggaga gaaaattttg tcctcttgct ttagagttgt gtgtaaatca aggaagccat      1476
122 cattaaattg ttttatttct ctc
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126 <211> LENGTH: 183
127 <212> TYPE: PRT
128 <213> ORGANISM: Homo sapiens
130 <400> SEQUENCE: 2
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133 1          5          10          15
136 Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile
137          20          25          30
140 Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val
141          35          40          45

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144 Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val
145      50      55      60
148 Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr
149 65      70      75      80
152 Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu
153      85      90      95
156 Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val
157      100      105      110
160 Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn
161      115      120      125
164 Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ser
165      130      135      140
168 Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala
169 145      150      155      160
172 Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe
173      165      170      175
176 Asp Arg His Lys Met Leu Ser
177      180

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180 &lt;210&gt; SEQ ID NO: 3

181 &lt;211&gt; LENGTH: 1828

182 &lt;212&gt; TYPE: DNA

183 &lt;213&gt; ORGANISM: Homo sapiens

185 &lt;220&gt; FEATURE:

186 &lt;221&gt; NAME/KEY: CDS

187 &lt;222&gt; LOCATION: (83)..(487)

188 &lt;223&gt; OTHER INFORMATION:

W--&gt; 191 &lt;400&gt; 3

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194 gggcgacgtg cccgcttcca aa atg gcg gcg gcg gta tct ggt gcg ctt      112
195      Met Ala Ala Ala Ala Val Ser Gly Ala Leu
196      1      5      10
198 ggc cgg gcg ggc tgg agg ctc ctg cag ctg cga tgc ctg ccc gtg gcc      160
199 Gly Arg Ala Gly Trp Arg Leu Leu Gln Leu Arg Cys Leu Pro Val Ala
200      15      20      25
202 cgt tgc cga caa gcc ctg gtg ccg cgt gcc ttc cat gct tca gct gtg      208
203 Arg Cys Arg Gln Ala Leu Val Pro Arg Ala Phe His Ala Ser Ala Val
204      30      35      40
206 ggg cta agg tct tca gat gag cag aag cag cag cct ccc aac tca ttt      256
207 Gly Leu Arg Ser Ser Asp Glu Gln Lys Gln Gln Pro Pro Asn Ser Phe
208      45      50      55
210 tct cag cag cat tct gag aca cag ggc gca gaa aaa cct gat cca gag      304
211 Ser Gln Gln His Ser Glu Thr Gln Gly Ala Glu Lys Pro Asp Pro Glu
212      60      65      70
214 tct tct cat tca ccc ccc agg tat aca gac cag ggc ggc gag gag gag      352
215 Ser Ser His Ser Pro Pro Arg Tyr Thr Asp Gln Gly Gly Glu Glu Glu
216 75      80      85      90
218 gag gac tat gaa agt gag gag cag ttg cag cac cgc atc ctg acg gca      400
219 Glu Asp Tyr Glu Ser Glu Glu Gln Leu Gln His Arg Ile Leu Thr Ala
220      95      100      105

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Input Set : A:\217925US0XPCT.txt

Output Set: N:\CRF4\04032003\J030269A.raw

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222 gcc ctt gag ttt gtg ccc gcc cac ggg tgg aca gca gag gcg att gca      448
223 Ala Leu Glu Phe Val Pro Ala His Gly Trp Thr Ala Glu Ala Ile Ala
224          110          115          120
226 gaa gga gcc cag gtg tgt ata ggt gag ggt ggg gcc acc taaccaagat      497
227 Glu Gly Ala Gln Val Cys Ile Gly Glu Gly Gly Ala Thr
228          125          130          135
230 gagccaggat ggagtcacac caggcagagc ggggggcctc atgccttctt ccagtctagc      557
232 tcagagcccc tcacagctgc aagattgact ggtttttttc ccccaatagg gtggaactgg      617
234 ctttattttg tagttataaa gaacatacca tggagttggt tcttgggagt tgtgttctaa      677
236 aggcaatcta ttaggcaaga attgtctgtg atcaaaactc ccatgtttca ttgactctaa      737
238 gatgccattg gttgtaagaa gcatcatttt laaalycatc agtaaaaaag aaaacatact      797
240 gcccttcgaa ctatgacaaa gcacttctgt gattcacact gattttttaa aatgaaaaat      857
242 atatctgcat cttagaatta atgacatatg gtgtttgaaa accccaaga aggcaccact      917
244 ttggagacca acacatctta ttttcccaga aactctaata gcattttctg cattagtaca      977
246 gactgctgct ttagattagg cagcaggctc atgttcaggc catgtttag agaatcctcc      1037
248 agcatagcaa gataccatcc tccaagagac tgaggggatg acagagttgc atcttccatc      1097
250 ccaggcttgc tgcagggcac ctacccatgg acaatgggca aggttgctgc tttactgaaa      1157
252 ttttaactgtt atttccttgt cttctctcac tcccaagtgc acatttggtg acagaagtct      1217
254 cattagttaa atgtgggtgc tctgactcca ctgtaggctc attgtgaaaa ctgaacaata      1277
256 caaacaataa taaaaaagaa tgtagaaaac acctataatc acaccaaaga tcatactatc      1337
258 aacatttatg cctagatctt tocaattaaa accctttata tgattcattc tttaaatgtt      1397
260 tattgagcaa ataattgtcc ctaggcactg tgctagtcca agagacatga caggggtcaa      1457
262 agtgggtcaag atggatctgc ttctgacctg tgttgagctt ccagtctagc aacattaata      1517
264 aaatatatac aaatgtttac ttagaagatg tggttaagtgc tatcaaggaa aggtgctgtt      1577
266 gggctgtata atggaggac ccgatcatta gatcagggtc cagctgcgag attgactggt      1637
268 ttctttccct caatagggtg gaaatggctt tattttgtgg atataaaagt aatgaacct      1697
270 ggaattggtt cttgagagtt gtgttctaaa ggcaacctat tggcaagaat tgtctgtgat      1757
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274 agtacatcag t
277 <210> SEQ ID NO: 4
278 <211> LENGTH: 135
279 <212> TYPE: PRT
280 <213> ORGANISM: Homo sapiens
282 <400> SEQUENCE: 4
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285 1          5          10          15
288 Leu Leu Gln Leu Arg Cys Leu Pro Val Ala Arg Cys Arg Gln Ala Leu
289          20          25          30
292 Val Pro Arg Ala Phe His Ala Ser Ala Val Gly Leu Arg Ser Ser Asp
293          35          40          45
296 Glu Gln Lys Gln Gln Pro Pro Asn Ser Phe Ser Gln Gln His Ser Glu
297          50          55          60
300 Thr Gln Gly Ala Glu Lys Pro Asp Pro Glu Ser Ser His Ser Pro Pro
301 65          70          75          80
304 Arg Tyr Thr Asp Gln Gly Gly Glu Glu Glu Asp Tyr Glu Ser Glu
305          85          90          95
308 Glu Gln Leu Gln His Arg Ile Leu Thr Ala Ala Leu Glu Phe Val Pro
309          100          105          110
312 Ala His Gly Trp Thr Ala Glu Ala Ile Ala Glu Gly Ala Gln Val Cys

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Input Set : A:\217925US0XPCT.txt

Output Set: N:\CRF4\04032003\J030269A.raw

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313          115          120          125
316 Ile Gly Glu Gly Gly Ala Thr
317          130          135
320 <210> SEQ ID NO: 5
321 <211> LENGTH: 1584
322 <212> TYPE: DNA
323 <213> ORGANISM: Homo sapiens
325 <220> FEATURE:
326 <221> NAME/KEY: CDS
327 <222> LOCATION: (100)..(1194)
328 <223> OTHER INFORMATION:
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334 tcgccccctg cccaccggg cggcgtagg gcggtcacg atg ctg ccg ccc tta 114
335                                     Met Leu Pro Pro Leu
336                                     1 5
338 ccc tcc cgc ctc ggg ctg ctg ctg ctg ctg ctc ctg tgc ccg gcg cac 162
339 Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu Leu Cys Pro Ala His
340                                     10 20
342 gtc ggc gga ctg tgg tgg gct gtg ggc agc ccc ttg gtt atg gac cct 210
343 Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro Leu Val Met Asp Pro
344                                     25 30 35
346 acc agc atc tgc agg aag gca cgg cgg ctg gcc ggg cgg cag gcc gag 258
347 Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala Gly Arg Gln Ala Glu
348                                     40 45 50
350 ttg tgc cag gct gag ccg gaa gtg gtg gca gag cta gct cgg ggc gcc 306
351 Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu Leu Ala Arg Gly Ala
352                                     55 60 65
354 cgg ctc ggg gtg cga gag tgc cag ttc cag ttc cgc ttc cgc cgc tgg 354
355 Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe Arg Phe Arg Arg Trp
356 70 75 80 85
358 aat tgc tcc agc cac agc aag gcc ttt gga cgc atc ctg caa cag gac 402
359 Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg Ile Leu Gln Gln Asp
360                                     90 95 100
362 att cgg gag acg gcc ttc gtg ttc gcc atc act gcg gcc ggc gcc agc 450
363 Ile Arg Glu Thr Ala Phe Val Phe Ala Ile Thr Ala Ala Gly Ala Ser
364                                     105 110 115
366 cac gcc gtc acg cag gcc tgt tct atg ggc gag ctg ctg cag tgc gcc 498
367 His Ala Val Thr Gln Ala Cys Ser Met Gly Glu Leu Leu Gln Cys Gly
368                                     120 125 130
370 tgc cag gcg ccc cgc tgg cgg gcc cct ccc cgg ccc tcc ggc ctg ccc 546
371 Cys Gln Ala Pro Arg Trp Arg Ala Pro Pro Arg Pro Ser Gly Leu Pro
372                                     135 140 145
374 ggc acc ccc gga ccc cct ggc ccc gcg ggc tcc ccg gaa ggc agc gcc 594
375 Gly Thr Pro Gly Pro Gly Pro Ala Gly Ser Pro Glu Gly Ser Ala
376 150 155 160 165
378 gcc tgg gag tgg gga ggc tgc ggc gac gac gtg gac ttc ggg gac gag 642
379 Ala Trp Glu Trp Gly Gly Cys Gly Asp Asp Val Asp Phe Gly Asp Glu
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**VERIFICATION SUMMARY**

PATENT APPLICATION: **US/10/030,269A**

DATE: 04/03/2003

TIME: 14:28:07

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Output Set: **N:\CRF4\04032003\J030269A.raw**

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L:331 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:328  
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L:841 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:838